

- 1 -

SEQUENCE LISTING

<110> Agriculture Victoria Services Pty Ltd AND Pig Research and Development Corporation AND Pfizer Products Inc.

<120> Novel lawsonia spp. gene and uses therefor IV

<130> p:\oper\mro\lawson-4.pct

<140>

<141>

<150> US 60/133,973

<151> 1999-05-12

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 502

<212> PRT

<213> Lawsonia intracellularis

<400> 1

Met Met Gly Ser Leu Phe Ile Gly Ala Thr Gly Met Lys Thr His Ser

1 5 10 15

Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile

20 25 30

Gly Tyr Lys Glu Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp

35 40 45

Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met

50 55 60

Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe

65 70 75 80

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85 90 95

Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
100 105 110

Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr
115 120 125

Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr
130 135 140

Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser
145 150 155 160

Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp
165 170 175

Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu
180 185 190

Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr
195 200 205

Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His
210 215 220

Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys
225 230 235 240

Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala
245 250 255

Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr
260 265 270

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Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr
275 280 285

Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val
290 295 300

Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln
305 310 315 320

Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala
325 330 335

Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu
340 345 350

Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg
355 360 365

Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln
370 375 380

Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly
385 390 395 400

Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala
405 410 415

Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr
420 425 430

Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr
435 440 445

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Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val

450

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460

Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe

465

470

475

480

Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys

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490

495

Ala Leu Glu Leu Lys Arg

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<210> 2

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<212> DNA

<213> Lawsonia intracellularis

<220>

<221> CDS

<222> (1)..(1506)

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Met Met Gly Ser Leu Phe Ile Gly Ala Thr Gly Met Lys Thr His Ser

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15

aca ggg ttg ggt act gtc tcc aat aat att gct aac gca aat acc att 96

Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile

20

25

30

ggg tat aag cag caa cag gta gtg ttt caa gac ctg ttt agt caa gat 144

Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp

35

40

45

- 5 -

tta gca ata ggt tct act gga agt cag ggg cca aac cag gct ggt atg 192
 Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met
 50 55 60

gga gca cag gtt gga agt gtt cgc aca att ttt aca cag ggt gct ttt 240
 Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe
 65 70 75 80

gaa cct ggc aat agt gta aca gat ctt gct att ggt gga aaa ggt ttt 288
 Glu ~~Pro~~ Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe
 95 90 95

ttt cag gtt aca tta gag gat aaa gta cac tat aca cga gca ggg aat 336
 Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
 100 105 110

ttt cgt ttt act caa gat ggt ttt tta aat gat cct agc gga ttt act 384
 Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr
 115 120 125

tta atg ggc tca aga ata tct aat aat cct aac ata aaa aag gaa acc 432
 Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr
 130 135 140

ctt gaa cca att cag tta gac ttt aat gat cct aca gta gca aag tct 480
 Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser
 145 150 155 160

cct gca aaa aca agt aca gca tta aac gct gtg gta aac ctt ggt gat 528
 Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp
 165 170 175

agt aca gat aaa aca caa agt gaa gct aat cca tac ttt gca ctt ctt 576
 Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu

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180	185	190	
gag agc tgg aaa gga aat gga aca cct cct att tct aca tca aac tac 624			
Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr			
195	200	205	
tca tat gca caa cct atg aga gta tat gat caa caa gga aat tct cac 672			
Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His			
210	215	220	
gat ata act gta tat ttt gat gga gca ccc tct tca aca gga agt aaa 720			
Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys			
225	230	235	240
aca ttt gaa tac ctt gta gct atg aat cct agt gaa gat gga agt gct 768			
Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala			
245	250	255	
gca tca gga aca gat agt gca ggt ctc tta atg tct gga act atg aca 816			
Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr			
260	265	270	
ttt tca agt aat ggc gaa tta aaa aat atg aca gct ttt act cct act 864			
Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr			
275	280	285	
ggc tct gca aca aaa gat tta aat gca tgg caa cca gca cca tta gtc 912			
Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val			
290	295	300	
aat ggt tta cca cag ttt tca gca aat ttt gtt ggt gca gga ata cag 960			
Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln			
305	310	315	320

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cct tta aca tta gac ttt gga att aaa agc caa cag aat atg tgg gca 1008

Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala

325

330

335

gga gct cca gca tcc gct gct gcc ata ggt aca gat att ggg aaa ttg 1056

Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu

340

345

350

cca tca atg atg cca ata caa aca tcc agc ggt aat tct aca gca aga 1104

Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg

355

360

365

aat gga tca tct tca aca aga aga tat agc caa gat ggt tat cct cag 1152

Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln

370

375

380

gga gat cta gta gat gtc aca att acc tct gaa ggg aaa tta caa ggt 1200

Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly

385

390

395

400

aag tat agt aat agt cag gtt gtt gat ttt tat aat att cct tta gca 1248

Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala

405

410

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cgc ttt aca agt gag gat gga tta aga cga gaa ggg aat aac cat tat 1296

Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr

420

425

430

tcc gca aca ctt gac tca ggt ggg cca gag ttt gga ttg cca gga aca 1344

Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr

435

440

445

tct aac tat gga aaa ctt agt gtg aat caa ctt gag act tct aac gta 1392

Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val

450

455

460

- 8 -

gac atg agc aga gaa atg gtt aet atg att att att caa cgt ggt ttt 1440
Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe
465 470 475 480

cag atg aat agt aaa tct gtt aca aca gca gac aca atg cta caa aaa 1488
Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys
485 490 495

gca ctt gaa cta aag cgt taa 1509
Ala Leu Glu Leu Lys Arg
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<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

<400> 3

ctatttttag gagatgttat c 21

<210> 4

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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tacaaaatta acaataaaat ac 22

- 9 -

<210> 5

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> 5

gcgaattcca tatgatgggg agtttggtta ttgntgcc

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<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

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gctctagaga ctagtcatat taacgcttta gttcaagtgc

40